APPENDIX I

VERSION WITH MARKINGS TO SHOW CHANGES MADE PURSUANT TO 37 CFR § 1.12(b)(iii)

In the Specification:

Paragraph beginning at page 12, line 15 has been amended as follows:

Figure 1 shows the nucleotide sequence (SEQ ID NO:1) of the λ73 cDNA and the deduced primary structure of Pet-1 (SEQ ID NO:2). The two sets of numbering on the right mark either the nucleotide sequence or amino acid residues. Translation termination codons flanking the open reading frame are marked by asterisks. The ETS domain is [shaded] contained within the dashed lines. Underlined amino-acid sequences within the ETS domain mark homologous region in other ETS-domains that were used to prepare primers for the degenerate PCR screen. Boxed residues indicate putative MAP kinase phosphorylation sites. A putative nucleotide binding P-loop is enclosed by an oval. A possible polyadenylation signal motif is shown in capital letters at the end of the nucleotide sequence.

Paragraph beginning at page 12, line 25 has been amended as follows:

Figure 2 show the alignment of various ETS-domain sequences. A) The first three letters of each ETS-domain factor designation shown on the left indicate an organism, e.g. DRO, *Drosophila melanogaster*, followed by the common gene name. Columns of more than 40% sequence identity are [shaded]in bold text. B) Parsimony analysis of sequences encoding different ETS domains. The phylogenetic tree demonstrates relative similarities among the ETS DNA binding domains of Pet-1, Ets-1 and members of the ERG subfamily. The available sequence for the Drosophila ETS-3 ETS domain is incomplete (Chen, T., *et al.*, "Isolation and characterization of five Drosophila genes that encode an ets-related DNA binding domain" *Dev. Biol.* 151:176-191, 1992). Branch lengths do not represent estimates of evolutionary distances between protein sequences.